

<!--StartFragment-->RESULT 5

HUMORF08

LOCUS HUMORF08 3694 bp mRNA linear PRI 24-JAN-2003

DEFINITION Homo sapiens KIAA0022 mRNA, complete cds.

ACCESSION D14664

VERSION D14664.1 GI:285952

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Nomura,N., Miyajima,N., Sazuka,T., Tanaka,A., Kawarabayasi,Y., Sato,S., Nagase,T., Seki,N., Ishikawa,K. and Tabata,S.

TITLE Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1

JOURNAL DNA Res. 1 (1), 27-35 (1994)

PUBMED 7584026

REFERENCE 2

AUTHORS Nomura,N., Miyajima,N., Sazuka,T., Tanaka,A., Kawarabayasi,Y., Sato,S., Nagase,T., Seki,N., Ishikawa,K. and Tabata,S.

TITLE Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)

JOURNAL DNA Res. 1 (1), 47-56 (1994)

PUBMED 7584028

REFERENCE 3 (bases 1 to 3694)

AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.

TITLE Direct Submission

JOURNAL Submitted (11-NOV-1992) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cDNAinfo@kazusa.or.jp, Tel:+81-438-52-3913)

FEATURES Location/Qualifiers

source 1. .3694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="male"
/cell_line="KG-1"
/cell_type="Myeloblast"

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5'UTR <1. .184
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CDS 185. .697
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3'UTR 698. .>3694
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ORIGIN

Query Match 98.8%; Score 3694; DB 5; Length 3694;
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Db	1 GCTCCGGGCCGCGCTGCCGCCTCTGCTGCCGTGCTGGGCCCTGCCGCTGCTGCCGT 60
Qy	107 CGCGGACTGTCTTCATCTACTGGATTCAAGACAGTTGTTACATTTCTCCA 166
Db	61 CGCGGACTGTCTTCATCTACTGGATTCAAGACAGTTGTTACATTTCTCCA 120
Qy	167 AGAAGCCATCAAAGTAGAAAGCATAGAGGATGTCAGAAAATCAGTGTACTGACCATGGAGC 226
Db	121 AGAAGCCATCAAAGTAGAAAGCATAGAGGATGTCAGAAAATCAGTGTACTGACCATGGAGC 180
Qy	227 GGACATGATAAGCATAACATAATGAAGAAGAAAATGCTTTTACTGGATACTTTGGAAAAA 286
Db	181 GGACATGATAAGCATAACATAATGAAGAAGAAAATGCTTTTACTGGATACTTTGGAAAAA 240
Qy	287 GCAATGGAAGGCCAGATGATATCCTACTAGGCATGTTTATGACACAGATGATCGAG 346
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Qy	347 TTTCAAGTGGTTGATAATTCAAATATGACATTGATAAGTGGCACAGCCAAGATGATGA 406
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Db	841	TGTGAAAAGCTTTAGGTCATAAAAAAACAGGTTAGAATGATCTTACATAA 900
Qy	947	TAGTGATTAAAGCATCCGTCAAAGGCAGAACATCTGCTACTTGAATGAAGGAAGCTAA 1006
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Qy	1007	AGCCCAGCAGATAAAAATAAAAGCCCAGCTATTGCTTGCCTGCTGTATCTCCCTA 1066
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Qy	1067	TTTAGTTGACCCACTTTAGTTATGTTATTAGTAACATGAATGGGAATAAGTGA 1126
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Qy	1127	TTTAAGTACATCCCACATTTAAATCTTGTAAATTGTTATTTTTGGCAGATAA 1186
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Qy	1187	TTCCTCTAGAATGTTATCTTTTGTATTAGATGAAGAAAATTCAACTTTAACAA 1246
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Qy	1247	CCCCACACCAATTAGTTCTTACACTTACACACACCATTATCACAAATGACTCAA 1306
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Qy	1367	ATAGAGAAAAGCTGGCAATTAGGTTAACACTTACATTTAGTGCCTTAAAGGATTTC 1426
Db	1321	ATAGAGAAAAGCTGGCAATTAGGTTAACACTTACATTTAGTGCCTTAAAGGATTTC 1380
Qy	1427	TCTCTGCCACCATACCTTTGTACTTCCCTATACAAGATGTATCTCATCTCTCAA 1486
Db	1381	TCTCTGCCACCATACCTTTGTACTTCCCTATACAAGATGTATCTCATCTCTCAA 1440
Qy	1487	GCATTATAAATTCTTCAATGACATGAAAAGTGTGCAAGCAGCAAAACCGAAGAAAAA 1546
Db	1441	GCATTATAAATTCTTCAATGACATGAAAAGTGTGCAAGCAGCAAAACCGAAGAAAAA 1500
Qy	1547	CACTTAAAGTACAACGTAGTGACAGTGATCAAAGTTTCAGTCATTATTGTACATT 1606
Db	1501	CACTTAAAGTACAACGTAGTGACAGTGATCAAAGTTTCAGTCATTATTGTACATT 1560
Qy	1607	AAGAAAAGGTGAAAATCATTTGGGAGTAAAAAAATGAAAAGCTGAAACGAGTAATT 1666
Db	1561	AAGAAAAGGTGAAAATCATTTGGGAGTAAAAAAATGAAAAGCTGAAACGAGTAATT 1620
Qy	1667	TCCTCACCATCAATAACCAAAACAGGAAAGATAAGAATGTATAAATTTCACGTAAAT 1726
Db	1621	TCCTCACCATCAATAACCAAAACAGGAAAGATAAGAATGTATAAATTTCACGTAAAT 1680
Qy	1727	TAGTCACGTACTTATCAATGGGGATACGTTCTAAGAAATGCAAGTTAGGGATCTT 1786
Db	1681	TAGTCACGTACTTATCAATGGGGATACGTTCTAAGAAATGCAAGTTAGGGATCTT 1740
Qy	1787	GTGTGAAAATCAGCTTGTATTACACAAACCCAGATGGTAGGCCCTTTGTCCCAAAC 1846

Db	1741	GTGTGAAAATCAGCTTGATTACACAAACCCAGATGGTAGAGCCTATTTGTCCAAAC	1800
Qy	1847	CTACACAGCATGTTACTGTGCTGAATCTGCAGACAATTGTAACACAATTTGTGTATC	1906
Db	1801	CTACACAGCATGTTACTGTGCTGAATCTGCAGACAATTGTAACACAATTTGTGTATC	1860
Qy	1907	TAAATATAGAAAAGGTACAGTAAAAATATGGTCACTAAGGAAACACTGTTCTATATGTG	1966
Db	1861	TAAATATAGAAAAGGTACAGTAAAAATATGGTCACTAAGGAAACACTGTTCTATATGTG	1920
Qy	1967	GTCCTTACTGACTGAAGTATACTGCTAGAACGCTGAGGCTCAAAGAAAAGTAATCCCT	2026
Db	1921	GTCCTTACTGACTGAAGTATACTGCTAGAACGCTGAGGCTCAAAGAAAAGTAATCCCT	1980
Qy	2027	CTTCTGAATCCACACCCCATCAATTATCTTACTTCTGGGAGATAGATAGATATAC	2086
Db	1981	CTTCTGAATCCACACCCCATCAATTATCTTACTTCTGGGAGATAGATAGATATAC	2040
Qy	2087	TATCTCACTAGCTTACTAATGGCAACAAAGTTCCAGCTGTGTAGTCTCTTTTATTGA	2146
Db	2041	TATCTCACTAGCTTACTAATGGCAACAAAGTTCCAGCTGTGTAGTCTCTTTTATTGA	2100
Qy	2147	CCACATGAATCGAAAACACTCATCACAAATTATGCCACTATCATTAATGAGACATGAGTA	2206
Db	2101	CCACATGAATCGAAAACACTCATCACAAATTATGCCACTATCATTAATGAGACATGAGTA	2160
Qy	2207	ACTAAAAAGTGTAGAAAACATTACAGTGCAGCTACATGGTACTGAAAATGCAGGCCATT	2266
Db	2161	ACTAAAAAGTGTAGAAAACATTACAGTGCAGCTACATGGTACTGAAAATGCAGGCCATT	2220
Qy	2267	ACACCAAGCTGTTACACAAAGCACAAGCATGCTCTGTAAAGAGCTTACATTTCTGAGATTT	2326
Db	2221	ACACCAAGCTGTTACACAAAGCACAAGCATGCTCTGTAAAGAGCTTACATTTCTGAGATTT	2280
Qy	2327	GTATAGTGATTGAGATGTCTATTTATTGTAGACTATTACTAATGTCAATATTGAA	2386
Db	2281	GTATAGTGATTGAGATGTCTATTTATTGTAGACTATTACTAATGTCAATATTGAA	2340
Qy	2387	CACTACCCCTGGAATTCTGCCTGGTTTCTACCCAAATTGTACCACTCCTTGAAAGAACT	2446
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Db	2461	TAAAGGGTAGGGTAGATTGGTAGGAAAGTGTAAAGTCCAACCTAAACCAACAGTCT	2520
Qy	2567	CAAACGTCTACAACATGTCATGCCATGAGGCCACTAGGCCACATGAGGCTATTTAAGTAA	2626
Db	2521	CAAACGTCTACAACATGTCATGCCATGAGGCCACTAGGCCACATGAGGCTATTTAAGTAA	2580
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Db	2581	TTAGTTAAAATCCAGTTTCAATTACATTAGCCACATTGTCAGTGTCAAATCACA	2640
Qy	2687	GGTGGTTAGTGGCTACTGTACTGGCAACATACATTATAGAACATTTCATTAGGAAG	2746
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Db	2761	TTTGTACATTTGATACCTAACCTAATGGCAGCTTCCAAA 	2820
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Qy	2927	AAGTGTATATATATATATATGCGGAGTCCTACTGTGCTGCC 	2986
Db	2881	AAGTGTATATATATATATGCGGAGTCCTACTGTGCTGCC 	2940
Qy	2987	TGGCTCGATCTGGCTCTCCAATCTCCGCTTGAGGTTCAAG 	3046
Db	2941	TGGCTCGATCTGGCTCTCCAATCTCCGCTTGAGGTTCAAG 	3000
Qy	3047	TCAGCCTCTTAGTAGCTGGGACCACAGACATCTGTACC 	3106
Db	3001	TCAGCCTCTTAGTAGCTGGGACCACAGACATCTGTACC 	3060
Qy	3107	ATTTTGGTAGAGACGGGTTTCGCCCCATATTGACTGG 	3166
Db	3061	ATTTTGGTAGAGACGGGTTTCGCCCCATATTGACTGG 	3120
Qy	3167	AAGTGTACACCCACCTTGGTCTCCAAAGTGTGGGATTAC 	3226
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Qy	3227	TTGGCTACATTTTCTTATATACCGAACATCTATAAC 	3286
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Qy	3287	TAGTAAGAGATAATTGGATTACACAGGCAGGTTGTTACT 	3346
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Qy	3347	CTGCTTCTTCAACATCTGGTCTAGCTAGTAATAACA 	3406
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Qy	3407	TCAGAATAACATTTAAACTACATTCTTAGAAAATGCATT 	3466
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Qy	3467	ATGGTCTTTGTTAGAATTAAAACGTATAACCAATGAA 	3526
Db	3421	ATGGTCTTTGTTAGAATTAAAACGTATAACCAATGAA 	3480
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